

PATENT
 USSN 09/990,080
 Docket: 018/258c
 Substitute Specification

SEQUENCE LISTING

<110> Morin, Gregg B.
 Geron Corporation

<120> Human Telomerase Catalytic Subunit Variants

<130> 018/258c

<140> 00/000,000

<141> 2001-00-00

<140> US 09/128,354

<141> 1998-08-03

<150> US 09/052,864

<151> 1998-03-31

<160> 21

<170> PatentIn Ver. 2.0

<210> 1

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<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (56)...(3454)

<223> human telomerase reverse transcriptase (hTERT) cDNA

<400> 1

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Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro
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Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu Val
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gcc ttc acc acc agc gtg cgc agc tac ctg ccc aac acg gtg acc gac	442
Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp	
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Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly	
130 135 140 145	
gac gac gtg ctg gtt cac ctg ctg gca cgc tgc gcg ctc ttt gtg ctg	538
Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu	
150 155 160	
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Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln	
165 170 175	
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Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro	
180 185 190	
cga agg cgt ctg gga tgc gaa cgg gcc tgg aac cat agc gtc agg gag	682
Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu	
195 200 205	
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Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly	
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Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly	
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Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala	
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His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val	
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Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu	
275 280 285	
tct ggc acg cgc cac tcc cac cca tcc gtg ggc cgc cag cac cac gcg	970
Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala	
290 295 300 305	
ggc ccc cca tcc aca tcg cgg cca cca cgt ccc tgg gac acg cct tgt	1018
Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys	
310 315 320	
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Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp	
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Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser	
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ccc tgg atg cca ggg act ccc cgc agg ttg ccc cgc ctg ccc cag cgc 1210
Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg
370 375 380 385

tac tgg caa atg cgg ccc ctg ttt ctg gag ctg ctt ggg aac cac gcg 1258
Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala
390 395 400

cag tgc ccc tac ggg gtg ctc ctc aag acg cac tgc ccg ctg cga gct 1306
Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala
405 410 415

gcg gtc acc cca gca gcc ggt gtc tgt gcc cgg gag aag ccc cag gcc 1354
Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly
420 425 430

tct gtg gcg gcc ccc gag gag gag gac aca gac ccc cgt cgc ctg gtg 1402
Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val
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Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val
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Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg
470 475 480

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His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu
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ggg aag cat gcc aag ctc tgg ctg cag gag ctg acg tgg aag atg agc 1594
Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser
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gtg cgg gac tgc gct tgg ctg cgc agg agc cca ggg gtt ggc tgt gtt 1642
Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val
515 520 525

cgg gcc gca gag cac cgt ctg cgt gag gag atc ctg gcc aag ttc ctg 1690
Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu
530 535 540 545

cac tgg ctg atg agt gtg tac gtc gtc gag ctg ctc agg tct ttc ttt 1738
His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe
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tat gtc acg gag acc acg ttt caa aag aac agg ctc ttt ttc tac cgg 1786
Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg
565 570 575

aag agt gtc tgg agc aag ttg caa agc att gga atc aga cag cac ttg 1834
Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu
580 585 590

aag agg gtg cag ctg cgg gag ctg tgg gaa gca gag gtc agg cag cat 1882
Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His
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aag cct gac ggg ctg cgg ccg att gtg aac atg gac tac gtc gtg gga Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly 630 635 640	1978
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tgg cgc acc ttc gtg ctg cgt gtg cgg gcc cag gac ccg ccg cct gag Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu 690 695 700 705	2170
ctg tac ttt gtc aag gtg gat gtg acg ggc gcg tac gac acc atc ccc Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro 710 715 720	2218
cag gac agg ctc acg gag gtc atc gcc agc atc atc aaa ccc cag aac Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn 725 730 735	2266
acg tac tgc gtg cgt cgg tat gcc gtg gtc cag aag gcc gcc cat ggg Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly 740 745 750	2314
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cag ccg tac atg cga cag ttc gtg gct cac ctg cag gag acc agc ccg Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro 770 775 780 785	2410
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ggc tcc atc ctc tcc acg ctg ctc tgc agc ctg tgc tac ggc gac atg Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met 835 840 845	2602
gag aac aag ctg ttt gcg ggg att cgg cgg gac ggg ctg ctc ctg cgt Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg 850 855 860	2650

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Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val	885	890	895	
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Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala	900	905	910	
ctg ggt ggc acg gct ttt gtt cag atg ccg gcc cac ggc cta ttc ccc				2842
Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro	915	920	925	
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Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp	930	935	940	945
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Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn	950	955	960	
cgc ggc ttc aag gct ggg aag aac atg cgt cgc aaa ctc ttt ggg gtc				2986
Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val	965	970	975	
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Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser	980	985	990	
ctc cag acg gtg tgc acc aac atc tac aag atc ctc ctg ctg cag gcg				3082
Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala	995	1000	1005	
tac agg ttt cac gca tgt gtg ctg cag ctc cca ttt cat cag caa gtt				3130
Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val	1010	1015	1020	1025
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Trp Lys Asn Pro Thr Phe Leu Arg Val Ile Ser Asp Thr Ala Ser	1030	1035	1040	
ctc tgc tac tcc atc ctg aaa gcc aag aac gca ggg atg tgc ctg ggc				3226
Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly	1045	1050	1055	
gcc aag ggc gcc gcc ggc cct ctg ccc tcc gag gcc gtg cag tgg ctg				3274
Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu	1060	1065	1070	
tgc cac caa gca ttc ctg ctc aag ctg act cga cac cgt gtc acc tac				3322
Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr	1075	1080	1085	
gtg cca ctc ctg ggg tca ctc agg aca gcc cag acg cag ctg agt cgg				3370
Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg	1090	1095	1100	1105
aag ctc ccg ggg acg acg ctg act gcc ctg gag gcc gca gcc aac ccg				3418

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Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro
 1110 1115 1120

gca ctg ccc tca gac ttc aag acc atc ctg gac tga tggccaccg 3464
 Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1125 1130

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 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
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Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
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Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
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Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
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Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
 115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg Arg Val
 130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
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Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
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Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
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195 200 205
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210 215 220
Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
225 230 235 240
Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
245 250 255
Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
260 265 270
Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
275 280 285
Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
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Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
305 310 315 320
Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
325 330 335
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340 345 350
Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
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Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
370 375 380
Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
385 390 395 400
Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
405 410 415
Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
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Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
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Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
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Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
465 470 475 480
Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
485 490 495

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Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
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 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
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 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
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 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
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 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
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 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
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 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
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 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
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 Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
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 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
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Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
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Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
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Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
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Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
 900 905 910

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 915 920 925

Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
 930 935 940

Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
 945 950 955 960

Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
 965 970 975

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 980 985 990

Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln
 995 1000 1005

Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
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Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
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Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
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Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
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Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
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Substitute Specification

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